WHAT IS CLAIMED IS:

1. An isolated nucleic acid comprising:

a) a polynucleotide that encodes a polypeptide of SEQ ID NO: 2, 4, or 6;

b) a polynucleotide amplified from a Zea mays nucleic acid library using the primers from Seq ID NO: 1, 3 or 5;

c) a polynucleotide amplified from a Zea mays nucleic acid library using a 5' primer comprising ATG GGN AAR TAY ATG (CGN or AGR) AAR and a 3' primer comprising Seq ID NO: 1, 3 or 5;

d) a polynucleotide amplified from a Zea mays nucleic acid library using a 5' primer comprising ATG GGN AAR TAY ATG (CGN or AGR) AAR and a 3' primer comprising the CDK binding region of Seq ID NO: 1, 3 or 5;

e) a polynucleotide comprising at least 20 contiguous bases of SEQ ID NO: 1, 3 or 5;

f) a polynucleotide comprising at least 20 contiguous bases of SEQ ID NO: 1, 3 or 5 and ATG GGN AAR TAY ATG (CGN or AGR) AAR;

g) a polynucleotide comprising at least 20 contiguous bases of the 3' coding region of SEQ ID NO: 1, 3 or 5;

h) a polynucleotide comprising at least 20 contiguous bases of the 3' coding region of SEQ ID NO: 1, 3 or 5 and at least some of the CDK binding region;

i) a polynucleotide encoding a maize CKI protein;

j) a polynucleotide having at least 82% sequence identity to SEQ ID NOS: 1, 3, or 5 wherein the % sequence identity is based on the entire coding sequence of SEQ ID NOS: 1, 3, or 5 and is determined by BLAST 2.0, using default parameters;

k) a polynucleotide comprising at least 25 nucleotides in length which hybridizes under low stringency conditions to a polynucleotide having the sequence set forth in SEQ ID NO: 1, 3 or 5, wherein the conditions include hybridization with a buffer solution of 30 % formamide, 1 M NaCl, 1% SDS at 37°C and a wash in 2X SSC at 50°C;

l) a polynucleotide comprising at least 25 nucleotides in length and is coding sequence which hybridizes under low stringency conditions to a polynucleotide having the sequence set forth in SEQ ID NO: 1, 3 or 5, wherein the conditions include hybridization with a buffer solution of 30 % formamide, 1 M NaCl, 1% SDS at 37°C and a wash in 2X SSC at 50°C;

m) a polynucleotide encoding a polypeptide having CKI activity comprising a polynucleotide having at least 68% sequence identity to SEQ ID NO.: 3, wherein the wherein the polynucleotide is other than from AC069145, and wherein the percent sequence identity is based on the sequence comprising the amino acid coding sequence and is determined by BLAST 2.0 using default parameters;

n) a maize polynucleotide encoding a polypeptide having CKI activity comprising a polynucleotide having at least 68% sequence identity to SEQ ID NO.: 3 and wherein the percent sequence identity is based on the sequence comprising the amino acid coding sequence and is determined by BLAST 2.0 using default parameters;

o) a polynucleotide encoding a polypeptide having CKI activity and at least 73% sequence identity to SEQ ID NO.: 4, wherein the wherein the polynucleotide is other than from AC069145, and wherein the percent sequence identity is based on the amino acid coding sequence and is determined by BLAST 2.0 using default parameters;

p) a polynucleotide complementary to a polynucleotide of (a) through (o).

2. The isolated nucleic acid of Claim 1 characterized by the sequence set forth in SEQ ID NO: 1,3 or 5.

3. The isolated nucleic acid of claim 1 adducted to a second nucleic acid sequence encoding a DNA-binding domain.

4. A vector comprising at least one nucleic acid of claim 1.

5. An expression cassette comprising at least one nucleic acid of claim 1 operably linked to a promoter, wherein the nucleic acid is in sense or antisense orientation.

6. A host cell containing at least one expression cassette of claim 5.

7. The host cell of claim 6, wherein said host cell comprises a bacterium, yeast cell, insect cell or plant cell.

8. A transgenic plant comprising at least one expression cassette of claim 5.

9. The transgenic plant of claim 8, wherein the plant is corn, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley, oil-seed *Brassica* and millet.

10. A seed from the transgenic plant of claim 8.

11. The seed of claim 10, wherein the seed is from corn, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley, oil-seed *Brassica* and millet.

12. An isolated protein comprising:

a) a polypeptide comprising at least 25 contiguous amino acids of SEQ ID NO: 2, 4, or 6 ;

b) a polypeptide which is a maize CKI protein;

c) a polypeptide comprising at least 55% sequence identity to SEQ ID NO: 2, 4, or 6, wherein the % sequence identity is based on the entire coding sequence and is determined by BLAST 2.0 using default parameters;

d) a polypeptide comprising at least 55% sequence identity to SEQ ID NO: 2, 4, or 6, wherein the polypeptide is other than that encoded by AC069145, wherein the % sequence identity is based on the entire coding sequence and is determined by BLAST 2.0 using default parameters;

e) a polypeptide comprising at least 55% sequence identity to SEQ ID NO: 2, 4, or 6, wherein the % sequence identity is based on the entire coding sequence and is determined by BLAST 2.0 using default parameters;

f) a polypeptide encoded by a nucleic acid of claim 1; and

g) a polypeptide characterized by SEQ ID NO: 2, 4, or 6.

13. A ribonucleic acid sequence encoding a protein of claim 12.

14. A method of modulating the activity of CDK in a plant comprising;

a) stably transforming a plant cell with a maize CKI polynucleotide operably linked to a promoter, wherein the polynucleotide is in sense or antisense orientation;

b) growing the plant cell under plant growing conditions to produce a regenerated plant capable of expressing the CKI expression product for a time sufficient to modulate CDK activity in the plant.

15. The method of claim 14, wherein the CKI polynucleotide is selected from those of claim 1.

16. The method of claim 14, wherein the plant is corn, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley, oil-seed *Brassica* and millet.

17. A method for providing differential growth in a plant comprising modulating CDK activity by the method of claim 14.

18. The method of claim 17, wherein the differential growth is a positive growth advantage.

19. The method of claim 14, wherein CDK activity is modulated downward.

20. A method for increasing crop yield, root size, plant growth, tassel size and/or ear size comprising modulating CDK activity by the method of claim 19.

21. The method of claim 14, wherein CDK activity is modulated upward.

22. A method for conferring male sterility comprising modulating CDK activity by the method of claim 21.

23. A method for modulating endoreduplication comprising modulating CDK activity in the endosperm of corn, sorghum, wheat, rice, barley and millet by the method of claim 14, wherein the promoter is an endosperm-preferred promoter.

24. The method of claim 14, wherein cell numbers are modulated in one or more tissues of a plant.

25. The method of claim 24, wherein the tissue comprises root, seed, tassel, ear, silk, stalk, embryo, flower, grain, germ, head, leave, stem, seed, trunk, meristem or fruit.

26. The method of claim 14, wherein the plant cells are quiescent cells.

27. The method of claim 26, wherein the cells are nucellus, endosperm, pericarp, meristematic or leaf cells.

28. A method for improving transformation frequencies comprising increasing the number of cells in cell division, by the method of claim 14, further comprising:
    a) transforming the plant cell with a second polynucleotide operably linked to a promoter, wherein the polynucleotide is in sense or antisense orientation; and
    b) growing the plant cell under plant growing conditions to produce a regenerated plant.

29. The method of claim 28, wherein the CKI polynucleotide is selected from those of claim 1.

30. The method of claim 28, wherein the maize CKI polynucleotide is in the antisense orientation.

31. The method of claim 28, wherein the plant cell is a meristem cell.

32. The method of claim 28, wherein the plant is corn, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley, oil-seed *Brassica* and millet.

33. A method for modulating the expression of CKI in plant cells comprising:
    a) introducing into a plant cell one or more interactors; and
    b) expressing the interactor for a time sufficient to modulate CKI expression in the plant cell.

34. The method of Claim 33, wherein CDK activity is influenced by the modulation of CKI expression.

35. The method of Claim 33, wherein the interactors comprise one or more of the following;

a) a polynucleotide of claim 1, operably linked to a promoter, wherein the polynucleotide is in sense or antisense orientation; or

b) a polypeptide of claim 12.

36. The method of claim 33, wherein a downward modulation of CKI expression by the interactor, increases the number of dividing cells.

37. A method for improving transformation frequencies comprising modulating CKI expression by the method of claim 33.

38. The method of claim 33, further comprising growing the plant cell under plant growing conditions to produce a stably regenerated plant.

39. A method for modulating the activity of CKI in plant cells comprising introducing into the plant cells one or more interactors capable of expressing the interactor for a time sufficient to modulate CKI activity in the plant cell.

40. The method of Claim 39, wherein CDK activity is influenced by the modulation of CKI activity.

41. The method of Claim 40, wherein the interactors comprise one or more of the following:

a) an antibody directed against maize CKI;

c) a pharmaceutical directed against CKI; or

d) a peptide that binds to CKI; or

e) an aptamer that binds to CKI.

42. The method of claim 39, wherein CKI is suppressed by the interactor, increasing the number of dividing cells.

43. A method for improving transformation frequencies comprising modulating the activity of CKI by the method of claim 39.

44. The method of claim 39, further comprising growing the plant cell under plant growing conditions to produce a stably regenerated plant.

45. A method for ectopic expression to modulate cell proliferation comprising:
    a) stably transforming a plant cell with an maize CKI polynucleotide operably linked to a promoter, wherein the polynucleotide is in sense or antisense orientation;
    b) growing the plant cell under plant growing conditions to produce a regenerated plant capable of ectopic expression of the maize CKI polynucleotide for a time sufficient to modulate cell proliferation in the plant.

46. The method of claim 45, wherein the modulated cells are involved in floral development, organ formation or branch/tiller initiation.

47. The method of claim 45, wherein the modulated cells are involved in fertility.

48. The method of claim 45, wherein the cell proliferation is inhibited.

49. A method for identifying maize CKI interacting proteins comprising adducting the nucleic acid sequence of claim 1 to a second nucleic acid sequence encoding a DNA-binding domain.

50. A method for improving transformation comprising:
    a) stably transforming a plant cell with a maize CKI polynucleotide operably linked to a promoter, wherein the polynucleotide is in sense or antisense orientation;

b) growing the transformed plant cell under plant growing conditions to produce a regenerated plant cell capable of expressing the CKI expression product for a time sufficient to modulate CDK activity in the transformed plant cell; and

c) transforming the transformed plant cell with a second polynucleotide operably linked to a promoter, wherein the polynucleotide is in sense or antisense orientation to produce a second transformed plant cell.

51. The method of Claim 50 further comprising growing the second transformed plant cell under plant growing conditions to produce a regenerated plant.

52. The method of Claim 50 wherein CKI expression product is present during transformation of the transformed plant cell with a second polynucleotide.

53. The method of Claim 50 wherein the plant cell is a maize plant cell.

54. The method of Claim 50 wherein CKI expression product is an antisense polynucleotide.

55. The method of Claim 50 wherein the maize CKI polynucleotide operably linked to a promoter is a non-adenovirus vector.

56. The method of Claim 50 wherein the transformation frequency is improved.

57. The method of Claim 50 wherein the transformation initiation frequency is improved.

58. The method of Claim 50 wherein the transformation frequency of second transformed plant cells is improved.

59. The method of Claim 50 wherein the second transformation is of immature embryos using *Agrobacterium*-mediated transformation.

60. The method of Claim 50 further comprising flanking the CKI polynucleotide with recombination sequences.

61. A method for improving transformation comprising:
    a) introducing into a plant cell one or more interactors;
    b) expressing one or more interactors for a time sufficient to modulate CKI expression in the plant cell;
    c) transforming the transformed plant cell with a polynucleotide operably linked to a promoter, wherein the polynucleotide is in sense or antisense orientation to produce a transformed plant cell; and
    d) growing the transformed plant cell under plant growing conditions to produce a regenerated plant.

62. The method of Claim 61 wherein the interactors comprise one or more of the following;
    a) an antibody directed against maize CKI;
    b) a pharmaceutical directed against CKI; or
    c) a peptide that binds to CKI; or
    d) an aptamer that binds to CKI.

63. The method of Claim 61 wherein cell divisions is transiently stimulated.

64. The method of Claim 61 wherein the interactor comprises an antisense oligonucleotide.

65. The method of Claim 64 wherein the oligonucleotide comprises ATG GGN AAR TAY ATG (CGN or AGR) AAR.

66. The method of Claim 50 and 61 wherein recovery of stable transformation events is increased.

67. The method of Claim 50 and 61 wherein transformation of recalcitrant genotypes is improved.

68. The method of Claim 50 and 61 wherein the growth of transgenic tissue is stimulated above wild-type levels.

69. A method of modulating the cell cycle comprising;

a) transforming a plant cell with a CKI polynucleotide of Claim 1 operably linked to a promoter;

b) growing the transformed plant cell under plant growing conditions to produce a regenerated plant cell capable of expressing the CKI expression product for a time sufficient to modulate CKI activity in the transformed plant cell.

70. The method of claim 69 wherein transformation is through a physical method.

71. The method of claim 69 wherein transformation is through *Agrobacterium*-mediated transformation.

72. The method of claim 69 further comprising growing the transformed plant cell under plant growing conditions to produce a regenerated plant.

73. A method for increasing callus growth rate comprising;

a) transforming a plant cell with a CKI polynucleotide of Claim 1 operably linked to a promoter;

b) growing the transformed plant cell under plant growing conditions to produce a regenerated plant cell capable of expressing the CKI

expression product for a time sufficient to increase the callus growth rate of transformed plant cell.

74. A method for increasing transformation frequency comprising;

a) transforming a plant cell with a CKI polynucleotide of Claim 1 operably linked to a promoter;

b) growing the transformed plant cell under plant growing conditions to produce a regenerated plant cell capable of expressing the CKI expression product for a time sufficient to increase transformation frequency in the transformed plant cell.

75. The method of claim 74 wherein the plant cell is recalcitrant to transformation.

76. A method of increasing cell growth rate comprising;

a) transforming a plant cell with a CKI polynucleotide of Claim 1 operably linked to a promoter;

b) growing the transformed plant cell under plant growing conditions to produce a regenerated plant cell capable of expressing the CKI expression product for a time sufficient to increase the cell growth rate in the transformed plant cell.

77. The method of claim 76 further comprising growing the transformed plant cell under plant growing conditions to produce a regenerated plant.

78. The method of claim 76 wherein the promoter is tissue-preferred, inducible, constitutive, environmentally-regulated, developmentally-regulated, cell-specific/selective or tissue-specific/selective.